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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.71318 Seconds

(Without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-19

Perfect score: 599

Sequence: 1 3MNAFQOKHIIKTPICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	579.5	96.7	111	1	RNPO_RANCA
2	445	74.3	111	1	LECS_RANCA
3	369.	61.6	111	1	RNPL_RANCA
4	267.5	44.7	104	1	R330_RANPI
5	154.5	25.8	145	1	ANG3_MOUSE
6	149.5	25.0	145	1	ANGR_MOUSE
7	136.5	22.8	145	1	ANGI_MOUSE
8	128.5	21.5	167	1	RNBR_BOVIN
9	125.5	21.0	124	1	RNBR_BOVIN
10	124.5	20.8	123	1	ANG2_BOVIN
11	123.5	20.6	124	1	RNP_PIG
12	123.5	20.6	151	1	RNBR_CARCA
13	123	20.5	146	1	ANGI_MIOIA
14	123	20.5	146	1	ANGI_SAISC
15	122.5	20.5	119	1	RNP_IGUG
16	122.5	20.5	141	1	RNBR_GIRCA
17	122.5	20.5	151	1	RNBR_AXIPR
18	120	20.0	146	1	ANGI_CERAE
19	120	20.0	147	1	ANGI_PONPY
20	118.5	19.8	123	1	ANGI_PIG
21	118.5	19.8	143	1	RNBR_SHEEP
22	118	19.7	122	1	RNP_MACRU
23	118	19.7	146	1	ANGI_AOTTR
24	117.5	19.6	124	1	RNP_ANTAM
25	117	19.3	146	1	ANGI_SAGE
26	115.5	19.3	128	1	RNP_MYOCO
27	115	19.2	146	1	ANGI_MACMU
28	114	19.0	148	1	ANGI_BOVIN
29	113.5	18.9	124	1	RNP_CAMDR
30	113	18.9	147	1	ANGI_HUMAN
31	113	18.9	147	1	ANGI_PANTR
32	112.5	18.8	128	1	RNP_HORSE
33	111.5	18.6	128	1	RNP_PROGU

34	110.5	18.4	124	1	RNP_RANCA	P00666	rangifer la
35	110.5	18.4	149	1	RNP_MOUSE	P00663	mus musculus
36	109.5	18.3	124	1	RNP_CARCA	P00664	capreolus c
37	109.5	18.3	148	1	RN14_MOUSE	Q913H1	mus musculus
38	109	18.2	125	1	ANG1_RABIT	P31347	oryctolagus
39	109	18.2	146	1	ANG1_PAPHA	Q8W04	papio hamad
40	108.5	18.1	128	1	RNPB_CAVPO	P00679	capra porce
41	107.5	17.9	124	1	RNP_GIRCA	P00662	giraffa cam
42	107.5	17.9	130	1	RNP_CRITO	P24717	cricketulus
43	106.5	17.8	124	1	RNP_BURBU	P00657	bubalus bub
44	106.5	17.8	148	1	RNP_PERLE	Q9WU5	peromyscus
45	106.5	17.8	149	1	RNP_ACOCA	Q9WU5	acomys cali

ALIGNMENTS

RESULT 1	ID	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (static acid-binding lectin) (SBL-C).				
OS	Rana catesbeiana (bull frog).				
OC	Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.				
OX	NCBI_Taxid=8400;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Egg;				
RA	MEDLINE=87299649; PubMed=3304421.				
RA	Tilani K., Takio K., Kawada M., Nitta K., Sakakibara F., Kawachi H.,				
RT	Takayanagi G., Hakomori S.;				
RT	"Amino acid sequence of static acid binding lectin from frog (Rana				
RT	catesbeiana) eggs.";				
RL	Biochemistry 26:2189-2194(1987).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.				
RC	MEDLINE=92220613; PubMed=1373237;				
RA	Liao Y.-D.;				
RT	"A pyrimidine-quanine sequence-specific ribonuclease from Rana				
RT	catesbeiana (bullfrog) oocytes.";				
RL	Nucleic Acids Res. 20:1371-1377(1992).				
RN	[3]				
RP	CHARACTERIZATION.				
RC	TISSUE=Egg;				
RA	MEDLINE=93192604; PubMed=8448385;				
RA	Nitta K., Oyama F., Sekiguchi K., Kawachi H.,				
RT	Takayanagi Y., Hakomori S., Tilani K.;				
RT	"Ribonuclease activity of static acid-binding lectin from Rana				
RL	catesbeiana eggs.";				
RL	Glycobiology 3:37-45(1993).				
RN	[4]				
RP	STRUCTURE BY NMR.				
RA	MEDLINE=98437383; PubMed=9761686;				
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;				
RT	"The solution structure of a cytotoxic ribonuclease from the frog				
RT	of Rana catesbeiana (bullfrog).";				
RL	J. Mol. Biol. 283:231-244(1998).				
CC	-I- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE				
CC	RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)				
CC	AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS				
CC	MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG				
CC	EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING				
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND				
CC	HUMAN ORIGIN.				
CC	-I- SUBUNIT: MONOMER.				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PIR; A27121; A27121.				

PDB: 1BC4: 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA. 1.
 DR ProDom: PD000535; RNaseA. 1.
 DR SMART: SM00092; RNase_Pc. 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC. 1.
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SQ SEQUENCE 111 AA: 12464 MW: 08C9E5F55729ECF4 CRC64;

Query Match 96.7%; Score 579.5; DB 1; Length 111;
 Best Local Similarity 96.4%; Pred. No. 3e-56;
 Matches 107; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 59
 DB 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 60
 OY 60 LSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAGIGRC 110
 DB 61 LSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAGIGRC 111

RESULT 2
 LECs_RANJA STANDARD: PRT: 111 AA.
 ID LECs_RANJA
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sialic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE-Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamiya T., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,
 RA Takayanagi Y., Tlcanl K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 RT eggs.";
 RT J. Biochem. 108:139-143(1990).
 RL -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC PIR: JX0120; JX0120.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA. 1.
 DR ProDom: PD000535; RNaseA. 1.
 DR SMART: SM00092; RNase_Pc. 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC. 1.
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97

FT DISULFID 94 111
 SQ SEQUENCE 111 AA: 12326 MW: FDEBDF3834ED679 CRC64;

Query Match 74.3%; Score 445; DB 1; Length 111;
 Best Local Similarity 76.6%; Pred. No. 1.2e-41;
 Matches 85; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

OY 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 58
 DB 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 60
 OY 59 VLSSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAGIGRC 109
 DB 61 VLSSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAGIGRC 111

RESULT 3
 RNPL_RANJA STANDARD: PRT: 111 AA.
 ID RNPL_RANJA
 AC P14626;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, Liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull. frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RA Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
 RT liver.";
 RT J. Biochem. 106:729-735(1989).
 RL -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC PIR: JX0085; JX0085.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA. 1.
 DR ProDom: PD000535; RNaseA. 1.
 DR SMART: SM00092; RNase_Pc. 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC. 1.
 KW Hydrolyase; Nuclease; Endonuclease.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 104 104
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SQ SEQUENCE 111 AA: 12461 MW: D64BA72456C10788 CRC64;

Query Match 61.6%; Score 369; DB 1; Length 111;
 Best Local Similarity 64.9%; Pred. No. 2.2e-33;
 Matches 72; Conservative 9; Mismatches 28; Indels 2; Gaps 2;

OY 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 58
 DB 1 QNMAFFQOKHIKPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGV-INLN 60
 OY 59 VLSSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAGIGRC 109
 DB 61 VLSSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAGIGRC 111

RESULT 4			
ID	RNA30_RANP1	STANDARD;	PTT; 104 AA.
AC	P22069;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	01-FEB-1995 (Rel. 31, Last annotation update)		
DE	P-30 protein (EC 3.1.27.-) (onconase).		
OS	Rana pipiens (Northern leopard frog).		
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
RN	NCBI_TaxID=6404;		
RP	SEQUENCE.		
RC	TISSUE=Embryo;		
RX	MEDLINE=91093131; Pubmed=1985896;		
RA	Ardelt W., Mikulski S.M., Shogen K.;		
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";		
RL	J. Biol. Chem. 266:245-251(1991);		
RN	(2)		
RP	3D-STRUCTURE MODELING.		
RX	MEDLINE=93066156; Pubmed=1438177;		
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,		
RT	James M.N.G.;		
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";		
RL	Proteins 14:392-400(1992).		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).		
RX	MEDLINE=9416079; Pubmed=9120892;		
RA	Mosimann S.C., Ardelt W., James M.N.G.;		
RT	"Refined 1.7 A x-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";		
RL	J. Mol. Biol. 236:1141-1153(1994).		
CC	-I- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY		
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR		
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH		
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.		
CC	-I- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).		
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
DR	PDB: 1ONC; 31-JUN-94.		
DR	InterPro: IPR001427; RNaseA.		
DR	Pfam: PF00074; rnasea; 1.		
DR	ProDom: PD000535; RNaseA; 1.		
DR	SMART: SM00092; RNase_Pc; 1.		
DR	PROSITE, PS00127; RNASE_PANCREATIC; 1.		
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.		
FT	MOD_RES	1	1
FT	ACT_SITE	10	10
FT	ACT_SITE	31	31
FT	ACT_SITE	37	37
FT	DISULFID	19	68
FT	DISULFID	30	75
FT	DISULFID	48	90
FT	DISULFID	37	104
FT	HELIX	3	10
FT	HELIX	11	12
FT	HELIX	19	22
FT	HELIX	23	24
FT	TURN	26	30
FT	TURN	33	38
FT	STRAND	33	38
FT	HELIX	41	48
FT	HELIX	49	50
FT	STRAND	35	58
FT	STRAND	53	70
FT	TURN	74	75
FT	STRAND	77	84
FT	STRAND	86	91
FT	TURN	92	93
FT	STRAND	94	101
SEQ	SEQUENCE	104 AA;	11845 MW; 22A753C2FE9566B4 CRC64;

[illegible]

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QY      87 ETNVCCKENOXYPVHF 103
Db      122 GFRITIIIGENGMPVHF 138

          || : ||| :||| |
RESULT 7
ANGI_MOUSE ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91025023; PubMed=2222456;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE-Serum;
RC MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Blochim. Biophys. Acta 1162:177-186(1993).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOENIN INDICES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sb.ch)
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DR EMBL: U2516; AAA91366.1; -.
DR PIR: A35932; A35932.
DR HSSP: P03950; 1A4Y.
DR MGD: MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ANGIOENIN.
FT PYROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.

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Query Match	Best Local Similarity	21.5%	Score 128.5	DB 1	Length 167
Matches 37	Conservative 17	Mismatches 44	Indels 23	Gaps 7	
DR	Prodom: PD000535: RNaseA: 1.				
DR	SMART: SM00092: RNase_Pc: 1.				
DR	PROSITE: PS00127: RNase_PANCREATIC: 1.				
KW	HydroLase: Nuclease: Endonuclease: Glycoprotein: Signal.				
FT	SIGNAL	1	26		
FT	CHAIN	27	167		
FT	ACT_SITE	38	38		
FT	ACT_SITE	67	67		
FT	ACT_SITE	145	145		
FT	DISULFID	52	110		
FT	DISULFID	66	121		
FT	DISULFID	84	136		
FT	DISULFID	91	98		
FT	CARBOHYD	88	88		
FT	CARBOHYD	155	155		
FT	CARBOHYD	159	159		
FT	CONFLICT	155	155		
SO	SEQUENCE	167 AA	18450 MW: 681CAAC3CC2PC459 CRC64:		
DR	Prodom: PD000535: RNaseA: 1.				
DR	SMART: SM00092: RNase_Pc: 1.				
DR	PROSITE: PS00127: RNase_PANCREATIC: 1.				
KW	HydroLase: Nuclease: Endonuclease: Glycoprotein: Signal.				
FT	SIGNAL	1	26		
FT	CHAIN	27	167		
FT	ACT_SITE	38	38		
FT	ACT_SITE	67	67		
FT	ACT_SITE	145	145		
FT	DISULFID	52	110		
FT	DISULFID	66	121		
FT	DISULFID	84	136		
FT	DISULFID	91	98		
FT	CARBOHYD	88	88		
FT	CARBOHYD	155	155		
FT	CARBOHYD	159	159		
FT	CONFLICT	155	155		
SO	SEQUENCE	167 AA	18450 MW: 681CAAC3CC2PC459 CRC64:		
DR	Prodom: PD000535: RNaseA: 1.				
DR	SMART: SM00092: RNase_Pc: 1.				
DR	PROSITE: PS00127: RNase_PANCREATIC: 1.				
KW	HydroLase: Nuclease: Endonuclease: Glycoprotein: Signal.				
FT	SIGNAL	1	26		
FT	CHAIN	27	167		
FT	ACT_SITE	38	38		
FT	ACT_SITE	67	67		
FT	ACT_SITE	145	145		
FT	DISULFID	52	110		
FT	DISULFID	66	121		
FT	DISULFID	84	136		
FT	DISULFID	91	98		
FT	CARBOHYD	88	88		
FT	CARBOHYD	155	155		
FT	CARBOHYD	159	159		
FT	CONFLICT	155	155		
SO	SEQUENCE	167 AA	18450 MW: 681CAAC3CC2PC459 CRC64:		
DR	Prodom: PD000535: RNaseA: 1.				
DR	SMART: SM00092: RNase_Pc: 1.				
DR	PROSITE: PS00127: RNase_PANCREATIC: 1.				
KW	HydroLase: Nuclease: Endonuclease: Glycoprotein: Signal.				
FT	SIGNAL	1	26		
FT	CHAIN	27	167		
FT	ACT_SITE	38	38		
FT	ACT_SITE	67	67		
FT	ACT_SITE	145	145		
FT	DISULFID	52	110		
FT	DISULFID	66	121		
FT	DISULFID	84	136		
FT	DISULFID	91	98		
FT	CARBOHYD	88	88		
FT	CARBOHYD	155	155		
FT	CARBOHYD	159	159		
FT	CONFLICT	155	155		
SO	SEQUENCE	167 AA	18450 MW: 681CAAC3CC2PC459 CRC64:		
DR	Prodom: PD000535: RNaseA: 1.				
DR	SMART: SM00092: RNase_Pc: 1.				
DR	PROSITE: PS00127: RNase_PANCREATIC: 1.				
KW	HydroLase: Nuclease: Endonuclease: Glycoprotein: Signal.				
FT	SIGNAL	1	26		
FT	CHAIN	27	167		
FT	ACT_SITE	38	38		
FT	ACT_SITE	67	67		
FT	ACT_SITE	145	145		
FT	DISULFID	52	110		
FT	DISULFID	66	121		
FT	DISULFID	84	136		
FT	DISULFID	91	98		
FT	CARBOHYD	88	88		
FT	CARBOHYD	155	155		

Best Local Similarity 29.8%; Pred. No. 1.2e-06;
Matches 34; Conservative 20; Mismatches 43; Indels 17; Gaps 6;

OY 6 FQOKH-----IKPIICNTIILNNIYVGGCKRVNFIISATVVAICTGV-INLN 58
DB 8 FQOHHDPPSSSSSSSSNPNCKNMMSR-NNTOGCKEKNFVHSLDVGAVGSOIWNK 66
OY 59 VLTSTRFOUNT-----CTRTSITPRP-CPYSSRTEFTNYICVCENO--YPVHF 103
DB 67 NGOTNKYOSNSTMTHTDCROTGSSKTPNCAYKASOEKHIIVACEGNPPVPHF 120

RESULT 12

RNRB_CAPCA

ID RNRB_CAPCA STANDARD: FRT; 151 AA.

AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Beutelman H.J., van der Munnik N., Kleideidam R.G., Furia A.,
RT "Secretory ribonuclease genes and pseudogenes in true ruminants";
RL Gene 212:259-268(1998).

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: Y11673; CAAT2371.1; -
CC HSP: P00656; ISRN: -
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; RNaseA_1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC DR PRODOM: PD000535; RNaseA; 1.
CC DR SMART: SM00092; RNaseA_Pc; 1.
CC DR PROSITE: PS00147; RNASE_PANCREATIC; 1.
CC KM Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
CC FT ACT_SITE 41 41 BY SIMILARITY.
CC FT DISULFID 26 84 BY SIMILARITY.
CC FT DISULFID 40 95 BY SIMILARITY.
CC FT DISULFID 58 110 BY SIMILARITY.
CC FT DISULFID 65 172 BY SIMILARITY.
CC FT CARBOHYD 126 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
CC FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
CC FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
CC SQ SEQUENCE 151 AA; 16971 MW; 392D0E6302F006A6 CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 151;

Best Local Similarity 28.6%; Pred. No. 1.5e-06;
Matches 34; Conservative 18; Mismatches 44; Indels 23; Gaps 6;

OY 4 ATRFOQHITK-----TPIICNTIILNNIYVGGCKRVNFIISATVVAICTGVINL 57
DB 6 AKFRROHMDSSSSSSNPNCKNMMSR-FMTGRCKPVTFVHESLDNVKAVCS--QK 61
OY 58 NVL-----STRFOUNTCTRTSITPRP-CPYSSRTEFTNYICVCENO--YPVHF 103
DB 62 NITCKHGOFPNGYOSNSTMTHTDCROTGSSKTPNCAYKASOEKHIIVACEGNPPVPHF 120

RESULT 13

ANGI_MIOTA

ID ANGI_MIOTA STANDARD: PRT; 146 AA.

AC Q8WN65;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
OS ANG OR RNASES.
ON Mipithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Mipithecus.
OX NCBI_TaxID=36231;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution";
RL Mol. Biol. Evol. 19:438-445(2002).

CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS. ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: AF041665; AML61647.1; -
CC KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
CC KW Protein synthesis inhibitor; Signal.
CC FT SIGNAL 1 24 BY SIMILARITY.
CC FT CHAIN 25 146 ANGIOGENIN.
CC FT MOD_RES 25 25 PYROGLUTAMINE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC FT ACT_SITE 37 37 BY SIMILARITY.
CC FT ACT_SITE 64 64 BY SIMILARITY.
CC FT ACT_SITE 138 138 BY SIMILARITY.
CC FT DISULFID 50 105 BY SIMILARITY.
CC FT DISULFID 63 116 BY SIMILARITY.
CC FT DISULFID 81 131 BY SIMILARITY.
CC SQ SEQUENCE 146 AA; 16486 MW; C8C2682D3F5C0061 CRC64;

Query Match 20.5%; Score 123; DB 1; Length 146;

Best Local Similarity 40.3%; Pred. No. 1.6e-06;
Matches 31; Conservative 9; Mismatches 29; Indels 8; Gaps 3;

OY 33 CKRVNFIISATVVAICTGVINLV-----LSTTRFOUNTCTRTSITPRP-PCPYSSR 85
DB 63 CKDINFHGNRRSIRAC-GDENGNDYGENLISRTPPQVTCNLRGSPRPCHRYRAT 121
OY 86 TETNYICVCENOYPVH 102
DB 122 AGFRNIVACENGLPVH 138

RESULT 14

ANGI_SAISC

ID ANGI_SAISC STANDARD: PRT; 146 AA.

AC Q8WN65;
DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG OR RNASE5.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918422; PubMed=11919285;
 RA Zhang J., Rosenberg H.F.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution."
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF441670; AAL61652.1;
 DR KJ Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KM Protein synthesis inhibitor; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 146 ANGIOGENIN.
 FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY
 FT ACT_SITE 37 37 SIMILARITY).
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DISULFID 30 103 BY SIMILARITY.
 FT DISULFID 63 116 BY SIMILARITY.
 FT DISULFID 81 131 BY SIMILARITY.
 SQ SEQUENCE 146 AA; 16387 MW; 2E0372D0C64F7B8 CRC64;
 Query Match 20.5%; Score 123; DB 1; Length 146;
 Best Local Similarity 36.7%; Pred. No. 1.6e-06;
 Matches 29; Conservative 10; Mismatches 28; Indels 12; Gaps 3;
 QY 33 CKRVNFTFISSATFKAICTGVINL-----VLSTRPOLNCTRTSTPR-PCPYS 83
 DB 63 CKREINTIHKNKASIKAIICG---NONGOPYNGNORISTSAFOYITICRHIGSPAPPCRYR 119
 OY 84 SRTETNYICVKNQYPAH 102
 DB 120 ATAGFRNIVIAECNGELPVH 138
 RESULT 15
 RNP_IGUIG
 ID RNP_IGUIG STANDARD; PRT; 119 AA.
 AC P80287;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 OS Iguana iguana (Common Iguana).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
 OX NCBI_TaxID=6517;

RN [1]
 RP SEQUENCE.
 RC TISSUE=pancreas;
 RX MEDLINE=94139745; PubMed=8307028;
 RA Zhao W., Beintema J.J., Hofsteenge J.;
 RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic
 RT ribonuclease."
 RL Eur. J. Biochem. 219:641-646(1994).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- FUNCTION: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSSP; P00656; 1LSQ.
 DR Interpro: IPR001427; RNaseA.
 DR Pfam: PF000074; RNaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_PC; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KM Hydrolyase; Nuclease; Endonuclease.
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT DISULFID 25 80 BY SIMILARITY.
 FT DISULFID 39 91 BY SIMILARITY.
 FT DISULFID 57 106 BY SIMILARITY.
 FT ACT_SITE 10 10 BY SIMILARITY.
 FT ACT_SITE 40 40 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;
 Query Match 20.5%; Score 122.5; DB 1; Length 119;
 Best Local Similarity 29.6%; Pred. No. 1.5e-06;
 Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 5;
 QY 1 QNATFEQKH-----IKTP-IICNTILDNNIYVGQCKRVNFTFISSATFKAIC-- 51
 DB 1 QDMSSFONKHIDYPTSSASNPNAVCDLMQOR-NLNPCKCKTRNTFVHASPSELDQVCGS 59
 OY 52 --TGVINLNVLSSTRPOLNCTRTSTPR-PCPYSRSTETNYICVKNQYPAH 103
 DB 60 GGTIVEDNLVDSNESFPLTDCKNVGTAPSSCKTNGTPKRRIRIACENNQPAH 114
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